Amendments to the Claims

Please amend claims as shown below in the List of Claims.

List of Claims

1-12. (Canceled)

13. (Currently amended) A process for the production of an L-amino acid chosen from the group consisting of L-threonine, L-isoleucine, L-valine, L-methionine, L-homoserine and L-lysine comprising:

a) fermenting a bacterium comprising an overexpressed endogenous DNA sequence encoding the galactose-proton symporter protein in said bacterium, in a fermentation medium under conditions suitable for the production of said L-amino acid, wherein:

i) said bacterium is of ~~the~~ an Enterobacteriaceae family;

ii) said galactose-proton symporter protein comprises the amino acid sequence of SEQ ID NO:4 and is encoded by the nucleotide sequence of SEQ ID NO:3;

iii) said L-amino acid is produced from glucose, saccharose, lactose, fructose, molasses, starch, cellulose or from glycerine and ethanol;

iv) said overexpression is achieved by increasing the copy number of said DNA or by operably linking said DNA to a promoter; and

b) allowing said L-amino acid to become enriched in said bacteria or said fermentation medium.

14. (Previously presented) The process of claim 13, wherein said galactose-proton symporter protein consists of the amino acid sequence of SEQ ID NO:4.

15. (Currently amended) The process of claim 14, wherein said DNA sequence encoding the galactose-proton symporter protein ~~comprises~~ consists of the nucleotide sequence of SEQ ID NO:3.

16. (Previously presented) The process of claim 13, wherein said DNA sequence encoding the galactose-proton symporter protein consists of the nucleotide sequence of SEQ ID NO:3.

17. (Previously presented) The process of claim 13, wherein overexpression is achieved by increasing the copy number of said DNA.

18. (Previously presented) The process of claim 13, wherein said L-amino acid is L-threonine.

19. (Previously presented) The process of any one of claims 13-16, further comprising isolating said L-amino acid along with some or all of the constituents of said fermentation medium and/or the biomass in said fermentation medium.

20. (Previously presented) The process of claim 19, wherein said L-amino acid is L-threonine.

21. (Previously presented) The process of claim 13, wherein said microorganism overexpresses one or more genes selected from the group consisting of:

a) the thrABC operon coding for aspartate kinase, homoserine dehydrogenase, homoserine kinase and threonine synthase;
b) the pyc gene coding for pyruvate carboxylase;
c) the pps gene coding for phosphoenolpyruvate synthase;
d) the ppc gene coding for phosphoenolpyruvate carboxylase;
e) the pntA and pntB genes coding for transhydrogenase,
f) the rhtB gene which imparts homoserine resistance;
g) the mqo gene coding for malate:quinone oxidoreductase;
h) the rhtC gene which imparts threonine resistance;
i) the thrE gene coding for threonine export protein;
j) the gdhA gene coding for glutamate dehydrogenase;
k) the glk gene coding for glucokinase;
l) the hns gene coding for DNA binding protein HLP-II;
m) the pgm gene coding for phosphoglucomutase;

n) the fba gene coding for fructose biphosphate aldolase;

o) the ptsH gene coding for phosphohistidine protein hexose phosphotransferase;

p) the ptsI gene coding for enzyme I in the phosphotransferase system;

q) the crr gene coding for the glucose-specific IIA component;

r) the ptsG gene coding for the glucose-specific IIBC component;

s) the lrp gene coding for a regulator in the leucine regulon;

t) the csrA gene coding for the global regulator Csr;

u) the fadR gene coding for a regulator in the fad regulon;

v) the iclR gene coding for a regulator in central intermediary metabolism;

w) the mopB gene coding for the 10 KDa chaperone;

x) the ahpC gene coding for the small sub-unit of alkyl hydroperoxide reductase;

y) the ahpF gene coding for the large sub-unit of alkyl hydroperoxide reductase;

z) the cysK gene coding for cysteine synthase A;

aa) the cysB gene coding for the regulator in the cys regulon;

bb) the cysJ gene coding for the flavoprotein in NADPH sulfite reductase;

cc) the cysI gene coding for haemoprotein in NADPH sulfite reductase;

dd) the cysH gene coding for adenylylsulfate reductase;

ee) the phoB gene coding for the positive regulator PhoB in the pho regulon;

ff) the phoR gene coding for the sensor protein in the pho regulon;

gg) the phoE gene coding for protein E in the outer cell membrane;

hh) the pykF gene coding for the pyruvate kinase I stimulated by fructose;

ii) the pfkB gene coding for 6-phosphofructokinase II;

jj) the malE gene coding for periplasmatic binding protein in maltose transport;

kk) the sodA gene coding for superoxidedismutase;

ll) the rseA gene coding for a membrane protein with anti-sigmaE activity;

mm) the rseC gene coding for a global regulator in the sigmaE factor;

nn) the sucA gene coding for the decarboxylase sub-unit of 2-ketoglutarate dehydrogenase;

00) the sucB gene coding for the dihydrolipoyl-transsuccinase E2 subunit of 2-ketoglutarate dehydrogenase;

pp) the sucC gene coding for the β-subunit of succinyl-CoA synthetase;

qq) the sucD gene coding for the α-subunit in succinyl-CoA synthetase;

rr) the adk gene coding for adenylate kinase;

ss) the hdeA gene coding for a periplasmatic protein with a chaperonin-like function;

tt) the hdeB gene coding for a periplasmatic protein with a chaperonin-like function;

uu) the icd gene coding for isocitrate dehydrogenase;

vv) the mglB gene coding for periplasmatic, galactose-binding transport protein;

ww) the lpd gene coding for dihydrolipoamide dehydrogenase;

xx) the aceE gene coding for the E1 component of pyruvate dehydrogenase complex;

yy) the aceF gene coding for the E2 component of pyruvate dehydrogenase complex;

zz) the pepB gene coding for aminopeptidase B;

aaa) the aldH gene coding for aldehyde dehydrogenase;

bbb) the bfr gene coding for the iron storage homoprotein;

ccc) the udp gene coding for uridine phosphorylase; and

ddd) the rseB gene coding for the regulator of sigmaE factor activity.

22. (Previously presented) The process of claim 13, wherein at least one gene in said microorganism is attenuated, said gene being selected from the group consisting of:

a) the tdh gene coding for threonine dehydrogenase;

b) the mdh gene coding for malate dehydrogenase;

c) the gene product of the open reading frame (ORF) yjfA;

d) the gene product of the open reading frame (ORF) ytfP;

e) the pckA gene coding for the enzyme phosphoenol-pyruvate carboxykinase;

f) the poxB gene coding for pyruvate oxidase;

g) the aceA gene coding for isocitrate lyase;

h) the dgsA gene coding for the DgsA regulator in the phosphotransferase system;

i) the fruR gene coding for fructose repressor;

j) the rpoS gene coding for the sigma^{38}-Factor;

k) the aspA gene coding for aspartate ammonium lyase; and

l) the aceB gene coding for malate synthase A gene.

23. (Currently amended) A process for the production of an L-amino acid chosen from the group consisting of L-threonine, L-isoleucine, L-valine, L-methionine, L-homoserine and L-lysine comprising:

a) fermenting a bacterium comprising an overexpressed endogenous DNA sequence encoding the galactose-proton symporter protein in said bacterium, in a

fermentation medium under conditions suitable for the production of said L-amino acid, wherein:

i) said bacterium is of ~~the~~ an Enterobacteriaceae family and transports glucose by a PEP-dependent phosphotransferase (PTS) pathway;

ii) said galactose-proton symporter protein comprises the amino acid sequence of SEQ ID NO:4;

iii) said L-amino acid is produced from glucose, saccharose, lactose, fructose, molasses, starch[[,]], cellulose or from glycerine and ethanol;

iv) said overexpression is achieved by increasing the copy number of said DNA or by operably linking said DNA to a promoter; and

b) allowing said L-amino acid to become enriched in said bacteria or said fermentation medium.

24. (Previously presented) The process of claim 23, further comprising isolating said L-amino acid along with some or all of the constituents of said fermentation medium and/or the biomass in said fermentation medium.

25. (Currently amended) The process of claim 24, wherein said bacterium is selected from the group consisting of: Escherichia coli H4581; ~~Escherichia coli KY10935;~~ Escherichia coli VNIIgenetika MG442; Escherichia coli VNIIgenetika M1; Escherichia coli VNIIgenetika 472T23 ~~(US-A-5,631,157)~~; Escherichia coli BKIIM B-3996; Escherichia coli kat 13; and Escherichia coli KCCM-10132.

26. (Previously presented) The process of claim 25, wherein said L-amino acid is L-threonine.